

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Mukherjee, Ranjan

5 (ii) TITLE OF INVENTION: Human Peroxisome
Proliferator
Activated Receptor γ

10 (iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon

15 (B) STREET: 633 West Fifth Street

(C) CITY: Los Angeles

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 90071

20 (v) COMPUTER READABLE FORM: *a*

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

(B) COMPUTER: IBM compatible

(C) OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

25 (D) SOFTWARE: WordPerfect (Version 5.1)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

30 (B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Warburg, Richard J.

35 (B) REGISTRATION NUMBER: 32,327

(C) REFERENCE/DOCKET NUMBER: 210/100

(ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (213) 489-1600

(B) TELEFAX: (213) 955-0440

(C) TELEX: 67-3510

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1641
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 1:

10 GAATTCCGGA CCCTCAACAC CACTCCCTCT TAGCCAATAT TGTGCCTATT 50
GCCATACTAG TCTTTGCGCC TCGGAAGCAG CGGTGGCCTA GCCCTACTAG 100
TCTCAATCTC CAACATATAT CGGCCTAGAC TACGTACATA ACCTAAACCT 150
ACTCCAATGC TAAAACTAAT CGTCCCTTTT CTCAAACGAG AGTCAGCCTT 200
TAACGAAATG ACCATGGTTG ACACAGAGAT GCCATTCTGG CCCACCAACT 250
15 TTGGGATCAG CTCCGTGGAT CTCTCCGTAA TGGAAGACCA CTCCCCTCC 300
TTTGATATCA AGCCCTTCAC TACTGTTGAC TTCTCCAGCA TTTCTACTCC 350
ACATTACGAA GACATTCCAT TCACAAGAAG AGATCCAGTG GTTGCAGATT 400
ACAAGTATGA CCTGAAACTT CAAGAGTACC AAAGTGCAAT CAAAGTGGAG 450
CCTGCATCTC CACCTTATTA TTCTGAGAAG ACTCAGCTCT ACAATAAGCC 500
20 TCATGAAGAG CCTTCCAACCT CCCTCATGGC AATTGAATGT CGTGTCTGTG 550
GAGATAAAGC TTCTGGATTT CACTATGGAG TTCATGCTTG TGAAGGATGC 600
AAGGGTTTCT TCCGGAGAAC AATCAGATTG AAGCTTATCT ATGACAGATG 650
TGATCTTAAC TGTCGGATCC ACAAAAAAAG TAGAAATAAA TGTCAGTACT 700
GTCGGTTTCA GAAATGCCTT GCAGTGGGGA TGTCTCATAA TGCCATCAGG 750
25 TTTGGGCGGA TGCCACAGGC CGAGAAGGAG AAGCTGTTGG CGGAGATCTC 800
CAGTGATATC GACCAGCTGA ATCCAGAGTC CGCTGACCTC CGGGCCCTGG 850
CAAAACATTT GTATGACTCA TACATAAAGT CCTTCCCGCT GACCAAAGCA 900
AAGGCGAGGG CGATCTTGAC AGGAAAGACA ACAGACAAAT CACCATTCTG 950
TATCTATGAC ATGAATTCCT TAATGATGGG AGAAGATAAA ATCAAGTTCA 1000
30 AACACATCAC CCCCCTGCAG GAGCAGAGCA AAGAGGTGGC CATCCGCATC 1050
TTTCAGGGCT GCCAGTTTCG CTCCGTGGAG GCTGTGCAGG AGATCAGAGA 1100
GTATGCCAAA AGCATTCCTG GTTTTGTAAA TCTTGACTTG AACGACCAAG 1150
TAACTCTCCT CAAATATGGA GTCCACGAGA TCATTTACAC AATGCTGGCC 1200
TCCTTGATGA ATAAAGATGG GGTTCATATA TCCGAGGGCC AAGGCTTCAT 1250
35 GACAAGGGAG TTTCTAAAGA GCCTGCGAAA GCCTTTTGGT GACTTTATGG 1300
AGCCCAAGTT TGAGTTTGCT GTGAAGTTCA ATGCACTGGA ATTAGATGAC 1350
AGCGACTTGG CAATATTTAT TGCTGTCATT ATTCTCAGTG GAGACCGCCC 1400
AGGTTTGCTG AATGTGAAGC CCATTGAAGA CATTCAAGAC AACCTGCTAC 1450

AAGCCCTGGA GCTCCAGCTG AAGCTGAACC ACCCTGAGTC CTCACAGCTG 1500
 TTTGCCAAGG TGCTCCAGAA AATGACAGAC CTCAGACAGA TTGTCACGGA 1550
 ACACGTGCAG CTACTGCAGG TGATCAAGAA GACGGAGACA GACATGAGTC 1600
 TTCACCCGCT COTGCAGGAG ATCTACAAGG ACTTGTACTA G 1641

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 494
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION : SEQ ID NO: 2

Met Leu Lys Leu Ile Val Pro Phe Leu Lys Arg Glu Ser Ala Phe
 5 10 15
 Asn Glu **Met** Thr **Met** Val Asp Thr Glu Met Pro Phe Trp Pro Thr
 20 25 30
 20 Asn Phe Gly Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His
 35 40 45
 Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser
 50 55 60
 Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe Thr Arg Thr
 25 65 70 75
 Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu Gln Glu
 80 85 90
 Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr Tyr
 95 100 105
 30 Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser
 110 115 120
 Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala
 125 130 135
 Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly
 35 140 145 150
 Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
 155 160 165

Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln
 170 175 180
 Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
 185 190 195
 5 Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu
 200 205 210
 Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser
 215 220 225
 10 Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile
 230 235 240
 Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr
 245 250 255
 Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn
 260 265 270
 15 Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr
 275 280 285
 Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln
 290 295 300
 20 Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu
 305 310 315
 Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp
 320 325 330
 Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr
 335 340 345
 25 Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu
 350 355 360
 Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys
 365 370 375
 30 Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys
 380 385 390
 Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
 395 400 405
 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val
 410 415 420
 35 Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
 425 430 435

Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala
440 445 450

Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu
455 460 465

5 His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met
470 475 480

Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
485 490